

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: November 25, 2000, 04:35:30 ; Search time 84.1 Seconds

(without alignments)  
B47.024 Million cell updates/sec

Title: US-09-373-230-1

Perfect score: 471

Sequence: 1 ACTTGGCCGACTTCACTG.....TCACAACTACATCAAGT 471

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620727 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.8  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/podata/1/ina/5A\_COMB.seq:\*

2: /cgn2\_6/podata/1/ina/5B\_COMB.seq:\*

3: /cgn2\_6/podata/1/ina/5C\_COMB.seq:\*

4: /cgn2\_6/podata/1/ina/5D\_COMB.seq:\*

5: /cgn2\_6/podata/1/ina/6\_COMB.seq:\*

6: /cgn2\_6/podata/1/ina/POTUS\_COMB.seq:\*

7: /cgn2\_6/podata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	470.6	99.9	471	4	US-09-502-535B-1	Sequence 1, Appli
2	470.6	99.9	471	4	US-09-908-005A-1	Sequence 1, Appli
3	27.4	52.5	519	3	US-08-896-605A-7	Sequence 7, Appli
4	27.4	52.5	519	3	US-08-896-501A-5	Sequence 5, Appli
5	27.4	52.5	1120	5	US-08-884-324-2	Sequence 2, Appli
6	127.8	27.1	11464	5	US-08-884-324-13	Sequence 13, Appli
7	127.8	27.1	28994	5	US-08-884-324-14	Sequence 14, Appli
8	112.2	25.9	2167	5	US-08-884-324-7	Sequence 7, Appli
9	75.6	16.1	134	5	US-08-884-324-4	Sequence 4, Appli
10	10.9	135	5	US-08-884-324-3	Sequence 3, Appli	
c	11	38.4	8.2	728	1	US-08-232-463-14
c	12	36.8	7.8	4731	4	US-08-488-706-2
c	13	36.8	7.8	4731	5	US-08-772-270A-9
c	14	34.4	7.3	10614	1	US-08-135-511-35
c	15	34.4	7.3	10614	2	US-08-187-453-35
c	16	33.8	7.2	8920	3	US-08-446-855A-1
c	17	33.2	7.0	4467	2	US-08-565-907A-1
c	18	33.2	7.0	4467	4	US-08-910-551B-1
c	19	33.2	7.0	4467	4	US-08-909-425A-1
c	20	32.6	6.9	4821	1	US-08-614-3
c	21	32.6	6.9	4821	2	US-08-316-397B-3
c	22	32.6	6.9	4821	3	US-09-034-306-3
c	23	32.6	6.9	4821	6	PCT-US93-09782-3
c	24	32.4	6.9	1326	5	US-09-100-391-1
c	25	32.4	6.9	3095	7	5231168-1
c	26	32	6.8	1431	2	US-08-451-715A-11

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.8

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/podata/1/ina/5A\_COMB.seq:\*

2: /cgn2\_6/podata/1/ina/5B\_COMB.seq:\*

3: /cgn2\_6/podata/1/ina/5C\_COMB.seq:\*

4: /cgn2\_6/podata/1/ina/5D\_COMB.seq:\*

5: /cgn2\_6/podata/1/ina/6\_COMB.seq:\*

6: /cgn2\_6/podata/1/ina/POTUS\_COMB.seq:\*

7: /cgn2\_6/podata/1/ina/backfile1.seq:\*

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.8

Maximum Match 100%

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Database : Issued\_Patents\_NA:\*

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3: /cgn2\_6/podata/1/ina/5C\_COMB.seq:\*

4: /cgn2\_6/podata/1/ina/5D\_COMB.seq:\*

5: /cgn2\_6/podata/1/ina/6\_COMB.seq:\*

6: /cgn2\_6/podata/1/ina/POTUS\_COMB.seq:\*

7: /cgn2\_6/podata/1/ina/backfile1.seq:\*

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.8

Maximum Match 100%

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3: /cgn2\_6/podata/1/ina/5C\_COMB.seq:\*

4: /cgn2\_6/podata/1/ina/5D\_COMB.seq:\*

5: /cgn2\_6/podata/1/ina/6\_COMB.seq:\*

6: /cgn2\_6/podata/1/ina/POTUS\_COMB.seq:\*

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Maximum DB seq length: 2000000000

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3: /cgn2\_6/podata/1/ina/5C\_COMB.seq:\*

4: /cgn2\_6/podata/1/ina/5D\_COMB.seq:\*

5: /cgn2\_6/podata/1/ina/6\_COMB.seq:\*

6: /cgn2\_6/podata/1/ina/POTUS\_COMB.seq:\*

7: /cgn2\_6/podata/1/ina/backfile1.seq:\*

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.8

Maximum Match 100%

Listing first 45 summaries

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Listing first 45 summaries

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Minimum DB seq length: 0

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0.8

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0.8

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0.8

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.8

Maximum Match 100%

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6: /cgn2\_6/podata/1/ina/POTUS\_COMB.seq:\*

7: /cgn2\_6/podata/1/ina/backfile1.seq:\*

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.8

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

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3: /cgn2\_6/podata/1/ina/5C\_COMB.seq:\*

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7: /cgn2\_6/podata/1/ina/backfile1.seq:\*

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.8

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/podata/1/ina/POTUS\_COMB.seq:\*

7: /cgn2\_6/podata/1/ina/backfile1.seq:\*

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.

TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..471  
 OTHER INFORMATION: /note= xaa in position 70 is Met or Thr  
 US-08-502-535B-1

Query Match 99.9%; Score 470.6; DB 4; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 2, 4e-132;  
 Matches 471; Conservative 0; Mismatches 0; Gaps 0;

1 AACITGGCGACTTCACTGTACAACCGCAGTAATCGGAATAATGACCAAGTCTCTC 60  
 1 AACITGGCGACTTCACTGTACAACCGCAGTAATCGGAATAATGACCAAGTCTC 60  
 61 TTCTGTTGACAAAGAACAGCCTGTTCCAGGATATGACTGATATTGATCAAAAGTGCCT 120  
 61 TTCTGTTGACAAAGAACAGCCTGTTCCAGGATATGACTGATATTGATCAAAAGTGCCT 120  
 121 GAACCCCAGACAGACTGATAATAATACATGTACAAGACAGTGAAGTAAGAGCAGTGGT 180  
 121 GAACCCCAGACAGACTGATAATAATACATGTACAAGACAGTGAAGTAAGAGCAGTGGT 180  
 181 GTGACCCCTCTGTGAAGGATAGTAAAGTCTACCCCTCTCTGTGAAGAACAGATCTT 240  
 181 GTGACCCCTCTGTGAAGGATAGTAAAGTCTACCCCTCTCTGTGAAGAACAGATCTT 240  
 181 GTGACCCCTCTGTGAAGGATAGTAAAGTCTACCCCTCTCTGTGAAGAACAGATCTT 240  
 181 GTGACCCCTCTGTGAAGGATAGTAAAGTCTACCCCTCTCTGTGAAGAACAGATCTT 240  
 241 TCCCTTGAGGAATGGATCCACCTGAAATAATGATGATAATAACAGTGTCTCATATT 300  
 241 TCCCTTGAGGAATGGATCCACCTGAAATAATGATGATAATAACAGTGTCTCATATT 300  
 241 TCCCTTGAGGAATGGATCCACCTGAAATAATGATGATAATAACAGTGTCTCATATT 300

301 TTTCAGAAAGTGTCCAGGACACAACAGATGGAGTTGAACTGTCTCACTGTATGAGGA 360  
 301 TTTCAGAAAGTGTCCAGGACACAACAGATGGAGTTGAACTGTCTCACTGTATGAGGA 360  
 361 CACTTCTGCTGGCAAAGGAGATGATGCTTCAAACTCATTCATCTGAAAGAAAAGGAT 420  
 361 CACTTCTGCTGGCAAAGGAGATGATGCTTCAAACTCATTCATCTGAAAGAAAAGGAT 420  
 421 GAAAATGGGATAAATCTGTATGTTCACTCTCACTTACATCAAAAGT 471  
 421 GAAAATGGGATAAATCTGTATGTTCACTCTCACTTACATCAAAAGT 471  
 421 GAAAATGGGATAAATCTGTATGTTCACTCTCACTTACATCAAAAGT 471

RESULT 2  
 US-08-908-005A-1  
 Sequence 1, Application US/08908005A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OKAMURA, Haruki  
 ; APPLICANT: TANIMOTO, Tadao  
 ; APPLICANT: TORIGOE, Kakuji  
 ; APPLICANT: KUNITAKA, Toshio  
 ; APPLICANT: TANIGUCHI, Mutsuko  
 ; APPLICANT: KOINO, Keizo  
 ; APPLICANT: KURIMOTO, Masashi  
 ; TITLE INVENTION: IFN-BETA PRODUCTION INDUCING PROTEIN AND  
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODY OF THE SAME  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC Compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0., Version #1.30

Query Match 99.9%; Score 470.6; DB 4; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 2, 4e-132;  
 Matches 471; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AACTTGGCCGACTTCACTGTACAACCGCAGTAATACGGATAATAATGACCAAGTCTC 60  
 QY 1 AACTTGGCCGACTTCACTGTACAACCGCAGTAATACGGATAATAATGACCAAGTCTC 60  
 DB 1 AACTTGGCCGACTTCACTGTACAACCGCAGTAATACGGATAATAATGACCAAGTCTC 60  
 DB 1 AACTTGGCCGACTTCACTGTACAACCGCAGTAATACGGATAATAATGACCAAGTCTC 60  
 QY 61 TTCTGTTGACAAAGAACAGCTGTGTTGAGGATATGACTGATATAAGTCAAGTGCAGT 120  
 DB 61 TTCTGTTGACAAAGAACAGCTGTGTTGAGGATATGACTGATATAAGTCAAGTGCAGT 120  
 QY 121 GAACCCCAGACAGACTGATAATAATACATGTACAAGACAGTGAAGTAAGAGCAGTGGT 180  
 DB 121 GAACCCCAGACAGACTGATAATAATACATGTACAAGACAGTGAAGTAAGAGCAGTGGT 180  
 QY 181 GTGACCCCTCTGTGAAGGATAGTAAAGTCTACCCCTCTCTGTGAAGAACAGATCTT 240  
 DB 181 GTGACCCCTCTGTGAAGGATAGTAAAGTCTACCCCTCTCTGTGAAGAACAGATCTT 240  
 QY 241 TCCTTGAGGAATGGATGCTTCACTCTCACTTACATCAAAAGT 471  
 DB 241 TCCTTGAGGAATGGATGCTTCACTCTCACTTACATCAAAAGT 471  
 QY 301 TTTCAGAAACGCTGTTCCAGGACACAAGATGGAGTTGAACTGTCTCATGTATGAGGA 360  
 DB 301 TTTCAGAAACGCTGTTCCAGGACACAAGATGGAGTTGAACTGTCTCATGTATGAGGA 360  
 QY 361 CACTTCTGCTGGATAAATCTGTATGTTCAACTTACATCAAAAGT 420  
 DB 361 CACTTCTGCTGGATAAATCTGTATGTTCAACTTACATCAAAAGT 420  
 QY 421 GAAAATGGGATAAATCTGTATGTTCACTCTCACTTACATCAAAAGT 471  
 DB 421 GAAAATGGGATAAATCTGTATGTTCAACTTACATCAAAAGT 471

RESULT 3  
 US-08-896-605A-7

Sequence 7, Application US/08896605A  
 Patent No. 5879942  
 GENERAL INFORMATION:  
 APPLICANT: TANIMOTO, Tadao  
 APPLICANT: KURIMOTO, Masashi  
 TITLE OF INVENTION: PROOCESSING ENZYME FOR POLYPEPTIDE  
 NUMBER OF SEQUENCES: 9  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NETMARK  
 STREET: 4149 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/896,605A  
 FILING DATE: 18 JULY 1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: J P 207,691/1996  
 FILING DATE: 19 JULY 1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: J P 156,062/1997  
 FILING DATE: 30 MAY 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: TANIMOTO-2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 579 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: 1 leader peptide  
 LOCATION: 1..108  
 IDENTIFICATION METHOD: S  
 NAME/KEY: mat peptide  
 LOCATION: 109..579  
 IDENTIFICATION METHOD: S  
 US-08-896-605A-7

Query Match 52.5%; Score 247.4; DB 3; Length 579;  
 Best Local Similarity 73.1%; Pred. No. 2.4e-65; 2;  
 Matches 343; Conservative 2; Mismatches 118; Indels 6; Gaps 2;

Qy 62 TCGTGTACAAAGACA --GCCTGTGTCGAGATGACTGATTCAGTGGCCA 118  
 Db 170 TCACTGACCAAGAAATCGCCGCTTAATGAGATGACTGATTCAGTGG 229  
 Qy 119 GTGAACCCCGAGCAGTGTAAATATCATGACAAAGAACAGTGAAGTAAAGGGACTGG 178  
 Db 230 ATGCACCCGGACGATATTATGATGAAATTCAGTAAAGATGAGCTGG 289  
 Qy 179 CTGTGACCCCTGTGAAAGGAGATAGAAAGGACCCCTGTGAAAGACAAGATCA 238  
 Db 290 CTGTGACCTCTGTGAAAGGACAAATTCATGTCCTGTGAGACAAATTA 349  
 Qy 239 TTTCCTTGAGGAAATGGATCCACTGTGAAATTGATGATATAAAAGTGTCTAT 298

RESULT 4  
 US-08-896-501A-5  
 ; Sequence 5, Application US/08896501A  
 ; Patent No. 5891633  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TANIMOTO, Tadao  
 ; APPLICANT: KURIMOTO, Masashi  
 ; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NETMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/896,501A  
 ; FILING DATE: 18-JUL-1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 213,267/1996  
 ; FILING DATE: 31-JAN-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BROWDY, Roger L.  
 ; REGISTRATION NUMBER: 25,618  
 ; REFERENCE/DOCKET NUMBER: TANIMOTO-3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; INFORMATION FOR SEQ ID NO: 5 :  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 579 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to mRNA  
 ; FEATURE:  
 ; NAME/KEY: leader peptide  
 ; LOCATION: 1..108  
 ; IDENTIFICATION METHOD: S  
 ; NAME/KEY: mat peptide  
 ; LOCATION: 109..579  
 ; IDENTIFICATION METHOD: S  
 US-08-896-501A-5

Query Match 52.5%; Score 247.4; DB 3; Length 579;  
 Best Local Similarity 73.1%; Pred. No. 2.4e-65; 2;  
 Matches 343; Conservative 2; Mismatches 118; Indels 6; Gaps 2;

Qy 299 TCTTTCAGAACTGTGTCGAGAC --ACAAAGATGAGATTCAGTGGCTCT 355  
 Db 410 TCTTTCAGAACTGTGTCGAGATGATAATAGATGCAATTGAACTCTCATACG 469

Qy 356 AGGACACTTCTGTGCTTGCAAAAGGAGATGATGCTTCAAACTCATCTGAAAGAAA 415  
 Db 470 AGGATACTTCTAGCTTGAGAAAGAGACCTTTAAACTCATTTGAAAGAAAAG 529

Qy 416 AGGATGAAATGGGATAAATCTGTAAATGTCACCTCTCAATTCTCA 464  
 Db 530 AGGATAATGGGGATAGATCTATAATGTTCACTGTTCAAACGAAAGA 578

LENGTH: 1120 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE: human

ORGANISM: human

TISSUE TYPE: liver

FEATURE: 5' UTR

LOCATION: 1..177

IDENTIFICATION METHOD: E

NAME/KEY: leader peptide

LOCATION: 178..285

IDENTIFICATION METHOD: S

NAME/KEY: mat peptide

LOCATION: 286..756

IDENTIFICATION METHOD: S

NAME/KEY: 3'-UTR

LOCATION: 757..1120

IDENTIFICATION METHOD: E

US-08-884-324-2

Query Match 52.5%; Score 247.4; DB 5; Length 1120;

Best Local Similarity 73.1%; Pred. No. 3..2e-65;

Matches 343; Conservative 2; Mismatches 118; Indels 6; Gaps 2

QY 2 ACTTGGCCGACTTCAGTGTACCCCTCCCTGTAAGAACAGATA 238

QY 350 TTTCCTTGAAGGATGATGATGAAATTGATGATCTCATAT 298

QY 299 TCTTTCAGAAAGCTGTCCAGGC --ACACAAGATGGACTTGAATCTCAGTGTATG 355

QY 410 TCTTCAGAGTGTCCAGGCATGATAAGCATGAACTCTCATACAG 469

QY 356 AAGGACACTTCTGCTGCCAANGGAAGATGATGCTTCAACTCATCTGAAAAAA 415

QY 470 AAGGATCTTCTAGTGTGAAATCTGATTTAAACTCATTTGAAAAARG 529

QY 416 AGATGAAGTGGATAATCTGTAACTGCTCACTACTACA 464

QY 530 AGGATGATTGGGGATAGATCTATAATGTTCAACCGAAGA 578

RESULT 5

Sequence 2, Application US/08884324

Patent No. 6050283

GENERAL INFORMATION:

APPLICANT: Takanori OKURA

APPLICANT: Kakuji TORIGOE

APPLICANT: Masashi KURIMOTO

TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE OF INDUCING THE PRODUCTION OF INTERFERON -

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

2TP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/884,324

FILING DATE:

CURRENT APPLICATION DATA:

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: JP 185,305/96

FILING DATE: 27-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: OKURA-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

SEQUENCE CHARACTERISTICS:

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NUMBER OF SEQUENCES : 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/884, 324  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 185, 305/96  
 FILING DATE: 27-JUN-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: OKURA=1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-282-5197  
 TELEFAX: 202-273-3228  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 11464 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: Genomic DNA  
 ORIGINAL SOURCE:  
 ORGANISM: human  
 TISSUE TYPE: Placenta  
 FEATURE:  
 NAME/KEY: 5' UTR  
 LOCATION: 1..3  
 IDENTIFICATION METHOD: E  
 NAME/KEY: leader peptide  
 LOCATION: 1454..1455  
 IDENTIFICATION METHOD: S  
 NAME/KEY: intron  
 LOCATION: 83..1453  
 IDENTIFICATION METHOD: E  
 NAME/KEY: leader peptide  
 LOCATION: 1454..1455  
 IDENTIFICATION METHOD: S  
 NAME/KEY: mat\_pept\_ide  
 LOCATION: 4866..4983  
 IDENTIFICATION METHOD: S  
 NAME/KEY: inttron  
 LOCATION: 4849..4865  
 IDENTIFICATION METHOD: S  
 NAME/KEY: mat\_pept\_ide  
 LOCATION: 6318..6451  
 IDENTIFICATION METHOD: S  
 NAME/KEY: inttron  
 LOCATION: 6452..11224  
 IDENTIFICATION METHOD: E  
 NAME/KEY: mat\_pept\_ide  
 LOCATION: 11225..11443  
 IDENTIFICATION METHOD: S  
 NAME/KEY: 3' UTR  
 LOCATION: 11444..11446

IDENTIFICATION METHOD: E  
US-08-884-324-13

Query Match 27.1%; Score 127.8; DB 5; Length 11464;  
Best Local Similarity 73.3%; Pred. No. 6.7e-29;  
Matches 178; Conservative 0; Mismatches 62; Indels 3; Gaps 1;

QY 225 TAAGAACAGATCATTCCTTGAGGAUATGGATCCACCTGAAATAATGATGATATA 284  
Db 11200 TTAGTATGTTTCTCTATAGGAAATGAACTTCCTCATACGATCAAAGATACAA 11259

Qy 285 AAGTGATCTATTCCTTCAGAACGCTTCAGGC--ACACAAAGATGGAGTTGA 341  
Db 11260 AATGACATCATATTCTTCAGAGAAGTGCTCCAGACATGATAATGAAATTGTA 11319

Qy 342 ATCTTCACTGTGTTGAAAGACATTCTGTGCTGCAAAGGAAGGTGATGCTTCAACT 401  
Db 11320 ATCTTCATCATAGAAAGGATACATTCTACCTGAAAAAGAGACCTTAACT 11379

Qy 402 CATTCTGAAAAAAAGATAAAATGGGATAAATCTGTAATGTCACCTCTACTT 461  
Db 11380 CATTTTGAAAAAGGAGGATGATATGGGGATAGATCTATAATGTCACIGTCAAAACGA 11439

Qy 462 ACA 464  
Db 11440 AGA 11442

RESULT 7  
US-08-884-324-14  
Sequence 14, Application US/08884324  
; Patent No. 6060283

GENERAL INFORMATION:  
APPLICANT: Takatori OKURA  
APPLICANT: Kakuji TORIGOE  
APPLICANT: Masahiro KURIMOTO  
TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE  
TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWNY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/0884,324  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 185,305/96  
FILING DATE: 27-JUN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWNY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: OKURA-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-5528  
SEQUENCE CHARACTERISTICS:  
LENGTH: 28994 base pairs  
TYPE: nucleic acid pairs  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA

ORIGINAL SOURCE: ;  
 ORGANISM: ; human  
 TISSUE TYPE: Placenta  
 FEATURE: ;  
 NAME/KEY: 5'UTR  
 LOCATION: 1..15606  
 IDENTIFICATION METHOD: E  
 NAME/KEY: leader Peptide  
 LOCATION: 15607..15685  
 IDENTIFICATION METHOD: S  
 NAME/KEY: Inttron  
 LOCATION: 15686..17056  
 IDENTIFICATION METHOD: E  
 NAME/KEY: leader Peptide  
 LOCATION: 17057..17068  
 IDENTIFICATION METHOD: S  
 NAME/KEY: Inttron  
 LOCATION: 17069..20451  
 IDENTIFICATION METHOD: E  
 NAME/KEY: leader Peptide  
 LOCATION: 20452..20468  
 IDENTIFICATION METHOD: S  
 NAME/KEY: mat peptide  
 LOCATION: 20469..20586  
 IDENTIFICATION METHOD: S  
 NAME/KEY: Inttron  
 LOCATION: 20587..21920  
 IDENTIFICATION METHOD: E  
 NAME/KEY: mat peptide  
 LOCATION: 21921..22054  
 IDENTIFICATION METHOD: S  
 NAME/KEY: Inttron  
 LOCATION: 22055..26827  
 IDENTIFICATION METHOD: E  
 NAME/KEY: mat peptide  
 LOCATION: 26828..27046  
 IDENTIFICATION METHOD: S  
 NAME/KEY: 3'UTR  
 LOCATION: 27047..28994  
 IDENTIFICATION METHOD: E  
 US-08-884-324-14

Query Match 27.1%; Score 127.8; DB 5; Length 28994;  
 Best Local Similarity 73.3%; Pred. No. 1e-28; Matches 178; Conserv. 0; Mismatches 62; Indels 3; Gaps 1;  
 Db 26803 TAGTAATGTCTTCTCTATAGGAATATGGATGATATAACA  
 Qy 225 TAAAGACAGATCATTTCTTGGAAATATGGATGATATAACA 284  
 Db 26803 TAGTAATGTCTTCTCTATAGGAATATGGATGATATAACA 26862  
 Qy 285 AAGTGATCTCATATTCTTCAGAAACCGTTCAGGAC--ACAACAAAGATGGAGTTGA 341  
 Db 26863 AAGTGACATCATATTCTTCAGAAAGTGTCCAGGACATGATAATTGCAATTGTA 26922  
 Qy 342 ATCTTCACTTGAAGGACACUTCTGCTGCCAAAGGAGATGATGCTTCAACT 401  
 Db 26923 ATCTTCACTCATGAAGGATACUTCTCAGCTGTGAAAGAGACCTTAAACT 26982  
 Qy 402 CATTCTGAAAAAAGGTGAAATGGGATAATCTGTAATGTTCACTCTCAACTT 461  
 Db 26983 CATTCTGAAAAAAGGTGAAATGGGGATGATCTAATGTCACGTCAAAACGA 27042  
 Qy 462 ACA 464  
 Db 27043 AGA 27045

Query Match 25.9%; Score 122; DB 5; Length 2167;  
 Best Local Similarity 75.7%; Pred. No. 1.8e-27; Matches 165; Conserv. 0; Mismatches 50; Indels 3; Gaps 1;  
 Db 1 GAAATGAATCTCTCTGATACATACAGGATACAAAAGTGCACATATCTTCAGAGA 60  
 Qy 250 GAAATGGATCCACCTGAAATAATTGATGATAATACAAGTGTCACTATCTTCAGAAA 309  
 Db 1 GAAATGAATCTCTCTGATACATACAGGATACAAAAGTGCACATATCTTCAGAGA 60  
 Qy 310 CGTGTTCAGGAC--ACAACAAAGATGGGTGAAATCTCAGTGTGAAAGACACTT 366  
 Db 61 AGTGTGTCAGGACATGATAATAGTGCATATGAAATTGAAATCTCATACAGGATACATT 120  
 Qy 367 CTTGCTTGCCTAAAGGAGATGATGCTTCAAATCTGAAATGATGAAAT 426  
 Db 121 CTAGCTTGTAAAGAGGAGAGACCTTTAACCTCATTTGAAAGAGGTGAAATTG 180  
 Qy 427 GGGATAAAATCTGTAATGTTCACTCTCACTAATTCA 464  
 Db 181 GGGATAGATCTATAATGTCACGTGTCACAAAGCAAGAAG 218

RESULT 8  
 US-08-884-324-7  
 Sequence 7, Application US/08884324  
 Patent No. 6060383  
 GENERAL INFORMATION:

RESULT 9  
 US-08-884-324-4  
 Sequence 4, Application US/08884324

Patent No. 6060283  
 GENERAL INFORMATION:  
 APPLICANT: takanori OKURA  
 APPLICANT: Kakaji TORIGOE  
 APPLICANT: Masahiro KURIMOTO  
 TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE OF INDUCING THE PRODUCTION OF INTERFERON-  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/884,324  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 185,305/96  
 FILING DATE: 27-JUN-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: OKURA=1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 134 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: Genomic DNA  
 ORIGINAL SOURCE: human  
 ORGANISM: human  
 TISSUE TYPE: placenta  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: 1..134  
 IDENTIFICATION METHOD: S  
 US-08-884-324-4

Query Match 16.1%; Score 75.6; DB 5; Length 134;  
 Best Local Similarity 72.7%; Pred. No. 4.5e-14;  
 Matches 96; Conservative 1; Mismatches 35; Indels 0; Gaps 0;

Qy 118 AGTGAACCCAGACCCAGTGTATATACATGTTAAAGACAGTGAAGTAAAGGACTG 177

Db 3 ATATGACACCCTGACCATATTTATATAAGTATATAACCTGAGCTATG 62

Qy 178 GCTGTGACCTCTGTGAAGGATAGTAAAYGTCACCCCTCTGTAAAGAACAGATC 237

Db 63 GCTGTAACCTATCTGTGAAGTGTGAGAAAATTCAACTCTCTGTGAGAACAAATT 122

Qy 238 ATTCCTTGTAG 249

Db 123 ATTCCTTAAAG 134

APPLICANT: takanori OKURA  
 APPLICANT: Kakaji TORIGOE  
 APPLICANT: Masahiro KURIMOTO  
 TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE OF INDUCING THE PRODUCTION OF INTERFERON-  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/884,324  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 185,305/96  
 FILING DATE: 27-JUN-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: OKURA=1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 135 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: Genomic DNA  
 ORIGINAL SOURCE:  
 ORGANISM: human  
 TISSUE TYPE: placenta  
 FEATURE:  
 NAME/KEY: exon  
 LOCATION: 1..135  
 IDENTIFICATION METHOD: S  
 US-08-884-324-3

Query Match 10.9%; Score 51.4; DB 5; Length 135;  
 Best Local Similarity 70.9%; Pred. No. 8.2e-07;  
 Matches 83; Conservative 0; Mismatches 31; Indels 3; Gaps 1;

Qy 2 ACTTTGGCGACTTACGTGAAACCGCAGTAATAGGAATAATAATGCAAGTTCTCT 61  
 Db 19 ACTTTGGCAAGCTGAATTCATCACTCATAGAAATTGTGACCAAGTTCTCT 78

Qy 62 TCTTGTACAAAGACA --GCCCTGTTGAGGATAGTACATATGTCAGTTCAGT 115  
 Db 79 TCTATGACCAAGGGAAATCGGCCTCTATTGAGATATGACTGTTGAGAG 135

RESULT 11  
 US-08-232-463-14/c  
 Sequence 14, Application US/08232463  
 Patent No. 5670367  
 GENERAL INFORMATION:  
 APPLICANT: DORNER, F.  
 APPLICANT: SCHEIFLINGER, F.  
 APPLICANT: FALKNER, F. G.  
 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
 NUMBER OF SEQUENCES: 52  
 CORRESPONDENCE ADDRESS:



GENERAL INFORMATION:  
 ; APPLICANT: MacInnes, Janet  
 ; APPLICANT: Ricciatti, Paul  
 ; APPLICANT: Mallard, Bonnie  
 ; APPLICANT: Rosendal, Soren  
 ; TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR  
 ; TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Beverskin & Parr  
 ; STREET: 40 King Street West  
 ; CITY: Toronto  
 ; STATE: Ontario  
 ; COUNTRY: Canada  
 ; ZIP: M5H 3Y2  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/772.270A  
 ; FILING DATE: December 23, 1996  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Gravelle, Michelle  
 ; REGISTRATION NUMBER: 40,261  
 ; REFERENCE/DOCKET NUMBER: 6580-81  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (416) 364-7311  
 ; TELEX: (416) 361-1398  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4731 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Actinobacillus pleuropneumoniae  
 ; US-08-772-270A-9

Query Match 7.8%; Score 36.8; DB 5; Length 4731;  
 Best Local Similarity 47.4%; Pred. No. 0.091;  
 Matches 110; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 211 TCTACCCCTCTGTAGAACAAATCATTCATTCTGAGAAATGGATCCACCTGAAT 270  
 Db 591 TCTATCCPAGCAAAAAGATCTGAAATATATATTAAAGGGAAATAAACAA 650

QY 271 ATGGATGATACAAAGTGTACATATCTCTCGAACACGTTCCAGGACACACAG 330  
 Db 651 AAAAGTGTGAAAGACATCTCTCGATAGAAGGTATACAGCTTACAT 710

QY 331 ATGGGATGAACTCTCACTGTAGAACACATCTCTCTCCAAAAGGAATGAT 390  
 Db 711 ATATCTTAAATGTCATATATAGAACACCTTATATAGAACACCTTGC 770

QY 391 GCTTCAAACCTATCTGAAAAAAGATGAAAATGGGATAATCTGAA 442  
 Db 771 ATCATAAATGCTCCCTACACAGGTGAAAATGGAAAACAAGTTA 822

RESULT 14 US-08-135-511-35/c  
 US-08-135-511-35/c Sequence 35, Application US/08135511  
 ; Sequence 35, Application US/08135511 ; Sequence 35, Application US/08187453  
 ; Patent No. 5753431 ; Patent No. 5753431

GENERAL INFORMATION:  
 ; APPLICANT: Chiang, John  
 ; TITLE OF INVENTION: Cholesterol 7 $\alpha$ -Hydroxylase Gene  
 ; NUMBER OF SEQUENCES: 35  
 ; NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington, D.C.  
 ; STATE: USA  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

GENERAL INFORMATION:  
 ; APPLICANT: Chiang, John  
 ; TITLE OF INVENTION: Cholesterol 7 $\alpha$ -Hydroxylase Gene  
 ; NUMBER OF SEQUENCES: 35  
 ; NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington, D.C.  
 ; STATE: USA  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

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: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/187,453
: FILING DATE: 28-JAN-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/135,488
: FILING DATE: 13-OCT-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/135,511
: FILING DATE: 13-OCT-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/135,510
: FILING DATE: 13-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: SANDERCOCK, Colin G.
: REGISTRATION NUMBER: 31,298
: REFERENCE/DOCKET NUMBER: 18748/188
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)672-5100
: TELEFAX: (202)672-5399
: TELEX: 904136
: INFORMATION FOR SEQ ID NO: 35:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10614 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-187-453-35

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Query Match          Score 34.4;  DB 2;  Length 10614;
Best Local Similarity 46.6%;  Pred. No. 0.68;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 110;  Conservative 0;  Mismatches 126;  Indels 0;  Gaps 0;
Db 10250 AACCTTACGAGACCTTGGATGGTTCAGGAGAACATGGATCACCCTGAAATATTGTGATATAAACAGT 288
Qy  229 ACAAGATCATTTCTTGGAGGAATGGATCACCCTGAAATATTGTGATATAAACAGT 288
Db 10190 AATCAGATAAAATTATTTAACCTTACATGTGGATGAAATAAACATTCTATTICAAGGTTA 10131
Qy  349 CTGTATGAGGACACTTCTGCTTGCCAAAAGGAATGATGCTTCAAACCTCATCTG 408
Db 10130 AAGCACAAATGTCCTTATTTCATTCTGAAAGTAGCTTAAGTTAAAGTACTGGTTT 10071
Qy  409 AAAAAAAGATGAAAAATGGGATAAAATCTGAAATGTCACCTCAACTTACA 464
Db 10070 AAAATATTACTTATATTGTGATATAAGATAAAAGATAATTACATATA 10015

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Search completed: November 25, 2000, 05:12:50  
 Job time: 2240 sec